



Best Local Similarity 38.5%; Pred. No. 1.4e-98;  
Matches 395; Conservative 167; Mismatches 285; Indels 179; Gaps 26;

QY 6 LLLLLLLPGIGTSTVLP-----ETLLVSTLDGLHAVSKRT 49  
Db 7 LFTFFLL-----FSSVICSTPGFRNDHESIGDEEKTSTLIVSTIDGRALDSET 61  
QY 50 GSIKTLKEDVLAQVTEVEEP-AFLPDNDGLTGLSKNNEGLTKLPETPELVQASP 108  
Db 62 GEIKTLODEEVLRSFSAVKQGFLLPNPLDGLYL--KNSLKLKLPENIPOLVHASP 118  
QY 109 CRSSDGLLYMKKODIMYVIDLTGEK-----QOTLSAFADSLCPST- 151  
Db 119 CKNGDILYAGSKKDYMGIDPKTGLKVEYLILNLSKILFLQVEFLTSASADRICPANO 178  
QY 152 -SLVLTGTEVITIMYDKTRRELKNNATFYDASLPDEGGYKMSHVSNDGLVIVD 210  
Db 179 KOTFLGRTGVSMFDEKRNKGTWNAFNDYSAHLLEPVNTWPKHYASSHGYLTED 238  
QY 211 SESGDVLIQVYASPVYAFYVQREGLRKVMHINAVETLRUTMGSGVGRITKMKYPF 270  
Db 239 RETGMREBODLKQVVALYLRLDGLKLPREVNGKETMEN--VAKNIFFVDMPIVL 295  
QY 271 -----PRETEAKSKLPTLYGVKYSTLSYASPSKV-HEGVAVPRGSTPLLEGPGTGG 323  
Db 296 GVNADPOTTLTNOFPALFVGESSFGLYALEALVDHQTITYSPKLLGPPLLEGAPAPA 355  
QY 324 VTIGDKGCV-----ITPSTDKFDPGLSKNKNLNLNLYLLGHHETP-LSAST 373  
Db 356 LTEMKEEYLLPPRRPIITNIPSTIKHTSDG-----EYLLGYHDPKMTMT 403  
QY 374 KMLEFPNNLKRHNVPADSEKKSFEVNLVDQTSENAPTYSRDVEEKPAPAPAP 433  
Db 404 IIPTRY-----VPGPK-----AIGSTIERPPQLGVE-----PKKH 438  
QY 434 E-----APVDSMLKQATILSTFLIGWAFITTYPLSMHQOQLOHQPO 480  
Db 439 EDTSFILLNNHPIPFATVTFALLVYIWCQ-----ROMQOQKST 483  
QY 481 KELEKILLOOQOQQLPRHPGDQADGELDTSGVSESSGTSPTSAPRASHLSG 540  
Db 484 SRMDSFEIVNN-----PGE-----SRSAOTSQOS----- 507  
QY 541 SSASKAGSSPSLEDDDEETSVYIVGKISCPKDYLGHGAGTIVYRGMDNRDVAVKR 600  
Db 508 NRGSGMANRKIEIEPEG---WMAVSGKLMYSPSDILGTGCGEYVYGTGFGREVAVKR 563  
QY 601 ILPECFSPADREVLRLSEDEHPNVIKFTCEKDRQFOYIAELCAATLOEYVEOKPRAH 660  
Db 564 VYSEFVKFAHREADLRSDHPIHRYECMESDSQFRLYALELCIASINDYVEQKEVOQ 623  
QY 661 ---LGLEPITLLOOTSGLAHLSNIYHRLDKPHNILLISPMNAHGKIKAMISDGLCKK 717  
Db 624 NVTIALRIT--MKQATDGLAHLSKIVHROMKPNVLTMAKSGEGRKAAVYSDGLCKK 681  
QY 718 LAVGRHSESR--RSGVPTEGMIAPEMLSECKENPTTVDFISAGCVYVVSSEGSHPF 775  
Db 682 VQPGNISIRGASLAGTADGMAPEVL---ISASTYVPDIFSLGCIFFYVLTSGTHP 738  
QY 776 GKSLQQRANILGACSLDCLRPKEHEDYIARELLEKMIAMOPKRPASNDYLKHPFESL 835  
Db 739 GKSLHQRANINYGEXTLKL-ADDLDMSLADLLISMLNVEPLNLTDAVLNHPFETIS 797  
QY 836 EKLOLFQDVSRIEKEISLDGRIKOLRGGRGAVYKMDMREINPTLDTLRKPTFYGG 895  
Db 798 EKRLATFSDVSQVKEKEDNSPVVARIETDARIYVCGWREICALEDKRKFTFYSGF 857  
QY 896 SVRDLRLAMRNKKHHYRELPAEVRTELTGTPDDEVCYFTSFPHLLATYPAHELCSHER 955  
Db 858 SVRDLRLAMRNKKHHYRELPAEVRTELTGTPDDEVCYFTSFPHLLATYPAHELCSHER 917  
QY 956 LFQRY 961  
::: ::

Db 918 VFKRY 923  
RESULT 2  
AC ID Y1EAST STANDARD: PRT: 1115 AA.  
AC P32361;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE SERINE/THREONINE-PROTEIN KINASE IREL PRECURSOR (EC 2.7.1.-).  
GN IREL OR ERN1 OR YHR079C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=9232627; PubMed=1625574;  
RA Nakawa J.-I., Yamashita S.;  
RT "IREL encodes a putative protein kinase containing a  
RT membrane-spanning domain and is required for inositol phototrophy in  
RT Saccharomyces cerevisiae."  
RL Mol. Microbiol. 6:1441-1446(1992).  
RN [2]  
RN [2] SEQUENCE FROM N.A.  
RP MEDLINE=93364990; PubMed=8358794;  
RA Mori K., Ma W., Gething M.J., Sambrook J.;  
RT "A transmembrane protein with a cdc2+/CDC28-related kinase activity  
RT is required for signaling from the ER to the nucleus."  
RL Cell 74:743-756(1993).  
RN [3]  
RN [3] SEQUENCE FROM N.A.  
RP STRAIN=5288C / AB972;  
RX MEDLINE=94378003; PubMed=8091229;  
RA Dunston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
RA Kuwaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
RA Lareille P., Louis E.J., Macri C., Maris E., Meneses S., Mouser L.,  
RA Nham N., Rifkin L., Riles L., St Peter H., Trevasis E., Vaughan K.,  
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
RA Vaudin M.;  
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
RT VIII."  
RN [4]  
RN [4] Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
RN [4] 265:2077-2082(1994).  
RP CHARACTERIZATION.  
RX MEDLINE=96272163; PubMed=8670804;  
RA Shamu C.E., Walter P.;  
RT "Oligomerization and phosphorylation of the Irelp kinase during  
RT intracellular signaling from the endoplasmic reticulum to the  
RT nucleus."  
RL EMBO J. 15:3028-3039(1996).  
CC -1- FUNCTION: DETECTS THE ACCUMULATION OF UNFOLDED PROTEINS. SEEMS TO  
CC BE INVOLVED IN THE UNFOLDED PROTEIN RESPONSE (UPR) PATHWAY BY  
CC INDUCING THE SPLICING OF HAC1.  
CC -1- SUBUNIT: MAY EXIST FIRST AS A MONOMER, AS THE CONCENTRATION OF  
CC UNFOLDED PROTEIN INCREASES. IT PROBABLY OLIGOMERIZES.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC  
CC RETICULUM.  
CC -1- PTM: AUTOPHOSPHORYLATED MAINLY ON SERINE RESIDUES.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -----  
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CC -----  
CC EMBL, Z11701; CAAT7763.1; -  
CC EMBL, L19640; AAA34489.1; -

DR EMBL: U10556; AAB68894.1; ALT\_INIT.  
DR PIR: S22629; S22629.  
DR PIR: A47541; A47541.  
DR HSSP: P24941; 1A01.  
DR SGP: S0001121; IRE1.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_kin\_actsite.  
DR Pfam: PF00069; pkinase.1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Transmembrane; Signal; Transferase; Serine/threonine-protein kinase;  
ATP-binding; Glycoprotein; Endoplasmic reticulum; Phosphorylation.  
FT SIGNAL 1 18  
FT CHAIN 19 526  
FT DOMAIN 19 526  
FT TRANSMEM 527 555  
FT DOMAIN 556 1115  
FT BINDING 674 980  
FT BINDING 702 702  
FT ACT\_SITE 797 797  
FT MOD\_RES 840 840  
FT MOD\_RES 841 841  
FT CARBOHYD 111 111  
FT CARBOHYD 213 213  
FT CARBOHYD 298 298  
FT CARBOHYD 397 397  
FT CONFLICT 368 368  
FT CONFLICT 626 626  
SQ SEQUENCE 1115 AA; 126975 MW; BD65D74E74365945 CRC64;  
ND -> S (IN REF. 1).  
ND -> KH (IN REF. 1).

Query Match 19.5%; Score 1004; DB 1; Length 1115;  
Best Local Similarity 27.18; Pred. No. 2.9e-53;  
Matches 305; Conservative 164; Mismatches 328; Indels 330; Gaps 42;

QY 32 LTFVTLGSLHVAVRKSGIKTKLED---PVLQV--PTHE--EPAPLPDNDGSLYT 84  
DB 122 ILIADVEGGLAVDRNRCHITISIEPENFQPIEIQSPRLIETETLIIIEFGDNITY 181  
QY 85 LGSKNNEGTLKLPETIPELVQASPCRSSDGI-----LYMKRKODIWIYIDL 131  
DB 182 FNA--HGGLOKPLISIRIVLSTSPHLKTNIVVNDGKIVEDEKYYTGSMTIMYTNML 239  
QY 132 TGEKOOTLSSAAD-----SLCPSTLLYIGRT--ETTMYDRK 169  
DB 240 NGE---IISAFGPGSKNGYFGSGVDCSPERIKRLQECENNIVIGKTFELGHSYDGA 295  
QY 170 TRELMNATYFPDYAASLPDEEDGYKMSHFVNSGDLVYVDSGDLVMIQVYAS--PVYA 228  
DB 296 S---YNTY-----STWQVNDLVPLAL 315  
QY 229 FYVWQREGIRKVMHINAVETLRVLTENSGEVG-RITKWKYPPPETEAKSKLPTLVYG 287  
DB 316 QNTFESKDGK-----CIAPFRKSLASDIDFRIARVSP----- 349  
QY 288 KSTSLVYSPSVHGVAVVPRGSLPLLEGQDTGVTG-----DKGECVITPSTD 339  
DB 350 -----TFP-----GLVGLPVDVNDLTFTNENILVPH-- 375  
QY 340 VAFDGG---LKSKNRLNLYRN---YMLLGHETPLASATKMLEFRPNLKRHNENYIP 392  
DB 376 -PFGNGDHESISKNV-YLDQTSNLSWFLSSONFPLVESAPISRYAS---DKRWYSS 430  
QY 393 ADSEKKSFEVY-----NLVDQTSNAPTVTSVDVEEKAHAHAPAEAPVD----- 438  
DB 431 IFEDETFENALMGVHOIYNNNEYDHLIYENYEKTSNLDITFK--YPLMLDSSVDITDLHO 488  
QY 439 -----SMKRNQATIIISTFLIGWAFITVPLSMHQOQLOHQOQKEL-EKIQ----- 487  
DB 489 NNEMNSLKEYS-----PEDLEAYRKRIHEQISRELDERKNQNSLLIK 530

QY 488 -----LLOQOQOOLPFHPGPDADGELDLTSGYSESSGTS 524  
DB 531 FGSIVYRIETGVFLFLFLICALLQRFKILPPLVYL--LSKIGFPEKEIPIVSKSLN 588  
QY 525 SPSTSPRASN-HSLCSGSSASKAGS-----SPSLQD---DQDETSTVIV----- 566  
DB 589 CPSSSEBNYTKPRDMKSGKGVVEGAVNDGSLKSEKNDNDADDDKSIDLTTEKKRRRG 648  
QY 567 -----GKISPCP-----KDVIGHAGETIYVRGMEDNDVAVKRILPEC 605  
DB 649 SNGCKKGRKRRIANIPNEQSLKMLVSEKILGYSGGVWFQSGFQGRPAVAKMLIDF 708  
QY 606 FEFADREVOLRESDEHPNVIYRFTCEKDRQFOYALIELCAATLQEVYEQKDFAHGLE- 664  
DB 709 CDIALMEIKLLNEDSDHPVIRYCYSETTDRFLYALIELCNLQDIVSKVNSDENLKL 768  
QY 665 -----PYLLQOTTSGLAHSLNLYHRDLAKHNILIS-----MPNAGKIRAMISD 711  
DB 769 QKEYNPISTLRIASGVANLHSLKILHRDLKPNILVSTSSRFTADQGTGAENLRILISD 828  
QY 712 FGLCKKLAVGRHSFSRSGVP--GTGGWIPEMLSDD----- 746  
DB 829 FGLCKKLDSGQSSFRITNLPNPSGTSGRAPDELLESNNIQCQVETHESSRHTVYSSDSF 888  
QY 747 ---CKENFTYVDFISACVFEYVYVSESGSHPGKSLQROANILGACSLD---CLHPERK 799  
DB 889 YPFTKRLTRISIDIFSMQCVFYILSKNHPGDKYSRESNIRIFSLDEMKCH-DR 947  
QY 800 HEDVARELIERKMIAMPQKRPANDVLRHPFWSLEKOLQFQVDSRIEKESLDGP-- 857  
DB 948 SLIAETDLSQIMIDHDLKPLTAMKVLHRPLFWPKSKLLEFLKVSDDLTEINRDPESA 1007  
QY 858 IYKOLENGRAVYVKM--DMENITDPLQDTLRKFRYTKGGSVDDLKRAMKKHHRELP 916  
DB 1008 LMKCKDAGSDPEYIPSGDWYFKDKTFMDNLERKRYHSSKMLDILKALKNHHFMDPE 1067  
QY 917 EYRETLGLPDDFCYFTSRPHLAHTYRAM-ELCSHRLRFPYVF 962  
DB 1068 DLALMGPPDGFYDFTKRPNLLIGVMIYKENISDQILREFLY 1114

RESULT 3  
ID CL4A\_CANAL STANDARD; PRT; 971 AA.  
AC 014427:  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE SERINE/THREONINE-PROTEIN KINASE CL4A (EC 2.7.1.-).  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Mucosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97411146; PubMed=9259554;  
RA Leberer E., Ziegelerbauer K., Schmidt A., Marcus D., Dignard D., Ash J.,  
Johnson L., Thomas D.Y.;  
RT "Virulence and hyphal formation of Candida albicans require the  
ste20p-like protein kinase Cacl4p.";  
RT Curr. Biol. 7:539-546(1997).  
CC -!- FUNCTION: ESSENTIAL FOR VIRULENCE AND MORPHOLOGICAL SWITCHING  
CC (HYPHAL FORMATION) OF C. ALBICANS.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 1 GBD DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.  
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